## AMENDMENTS TO THE SPECIFICATION

Please delete the paragraph beginning on page 5, line 17 and replace it with the following rewritten paragraph:

Figures 6A, 6B, and 6C 6A-F depict the nucleotide sequence (SEQ ID NO: 1) and predicted amino acid sequence (SEQ ID NO: 2) of hap gene. Putative -10 and -35 sequences 5' to the *hap* coding sequence are underlined; a putative *rho*-independent terminator 3' to the *hap* stop codon is indicated with inverted arrows. The first 25 amino acids of the protein, which are boxed, represent the signal sequence.

Please delete the paragraph beginning on page 5, line 17 and replace it with the following rewritten paragraph:

Figures 7A, 7B, 7C, 7D, 7E, 7F, 7G, and 7H 7A-J depict a sequence comparison of the *hap* product (SEQ ID NO: 2) and the cloned *H. influenzae* IgA1 proteases (SEQ ID NO: 3-6). Amino acid homologies between the deduced *hap* gene product and the *iga* gene products from *H. influenzae* HK368 (SEQ ID NO: 3), HK61 (SEQ ID NO: 6), HK393 (SEQ ID NO: 4), and HK715 (SEQ ID NO: 5) are shown. Dashes indicate gaps introduced in the sequences in order to obtain maximal homology. A consensus sequence for the five proteins is shown on the lower line. The conserved serine-type protease catalytic domain is underlined, and the common active site serine is denoted by an asterisk. The conserved cysteines are also indicated by asterisks.

Please delete the paragraph beginning on page 5, line 17 and replace it with the following rewritten paragraph:

Figure 11 depicts Figures 11A-D depict an alignment of the deduced amino acid sequence of HAP proteins obtained from various *H. influenzae* strains. The strains include N187 (SEQ ID NO: 7), TN106 (SEQ ID NO: 11) and 860295 (SEQ ID NO: 13).

Please delete the paragraph beginning on page 5, line 20 and replace it with the following rewritten paragraph:

~~Figure 12 depicts~~ <u>Figures 12A-B depict</u> Western blot of Hap proteins. Panel A shows outer membrane proteins, and panel B shows culture supernatants after precipitation with trichloroacetic acid. In each panel, lane 1 contains DB117/pGJB103 (vector), lane 2 contains DB117/pJS106 (encoding HapN187), lane 3 contains DB117/pHapP860295, and lane 4 contains DB117/pHapTN106. Immunoblotting was performed with guinea pig antiserum GP74, which was raised against purified $Hap_s$ from strain N187 and recognizes full-length Hap in outer membranes and $Hap_s$ in culture supernatants. Without being bound by theory, it is thought that the lower band in lane 3 of panel B presumably reflects autoproteolysis of multiple sites in Hap from strain P860925 (Fink et al; 2001).

Please delete the paragraph beginning on page 6, line 3 and replace it with the following rewritten paragraph:

~~Figure 16 depicts~~ <u>Figures 16A-B depict</u> the nucleotide sequence for NTHi strain 11 *hap* gene (SEQ ID NO: 8) (start codon to stop codon).

Please delete the paragraph beginning on page 6, line 7 and replace it with the following rewritten paragraph:

~~Figure 18 depicts~~ <u>Figures 18A-C depict</u> the nucleotide sequence for NTHi strain TN106 *hap* gene (SEQ ID NO: 10) (start codon begins at position 422, stop codon begins at position 4595).

Please delete the paragraph beginning on page 6, line 11 and replace it with the following rewritten paragraph:

~~Figure 20 depicts~~ <u>Figures 20A-C depict</u> the nucleotide sequence for NTHi strain 860295 *hap* gene (SEQ ID NO: 12) (start codon begins at position 430, stop codon begins at position 4738).

Please delete the paragraph beginning on page 6, line 15 and replace it with the following rewritten paragraph:

~~Figure 22 depicts~~ <u>Figures 22A-C depict</u> the nucleotide sequence for NTHi strain 3219B *hap* gene (SEQ ID NO: 14) (start codon begins at position 388, stop codon begins at position 4561).

Please delete the paragraph beginning on page 6, line 19 and replace it with the following rewritten paragraph:

~~Figure 24 depicts~~ <u>Figures 24A-C depict</u> the nucleotide sequence for NTHi strain 1396B *hap* gene (SEQ ID NO: 16)(start codon begins at position 313, stop codon begins at position 4546).